AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as follows: Please note that text to be deleted is indicated by double-bracketing only. Text in single bracketing should not be deleted.

Please delete the paragraph on page 4, line 36, through page 5, line 2, and replace it with the following paragraph:

Figure 12 (SEQ ID NOS: 24-27) shows the complete RNA DI-C cDNA sequence (See SEQ ID NO: 24) obtained by the sequencing of overlapping fragments of the *a, b, c,* and *d* cloning. RNA DI-C has kept four discontinuous parental genome regions: I, II, III and IV. The flanking sites of these regions are indicated with arrows. The translation of the three ORFs present in genome DI-C is indicated: chimeric ORF of 6.7 kb resulting from the fusion of discontinuous regions I and II in phase; the mini-ORF of three amino acids preceding it in phase; and the ORF, which initiates at the AUG of gene S. Highly homologous regions -- with the proteic domains described for other coronaviruses as those responsible for the polymerase and helicase activities, and metal ion binding sites -- appear shaded. CTAAAC transcription promoter sequences appear shaded. The overlapping area between ORFs 1a and 1b (41 nucleotides) appears shaded, the slippery sequence of the ribosome is underlined, and the ORF1a termination codon is in a box. In positions 637, 6397, and 6485, the specific changes with respect to the parental genome are indicated. The nucleotides present in the parental genome in these positions are indicated.

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Please delete the paragraph on page 5, lines 33-43, and replace it with the following paragraph:

Figure 15 shows the secondary and tertiary RNA structures in the overlapping zone between ORFs 1a and 1b in the RNA DI-C. (A) (SEQ ID NO: 28) Structure predicted when considering the region closest to the fork-like structure presenting complementarity to the nucleotides of the knot thus constituting the pseudoknot (nucleotides 2354 to 2358). The slippery sequence UUUAAAC is underlined. ORF1a termination codon is indicated in the box. (B) Schematic representation of this pseudoknot, which involves two sequence complementarity sections (stems: S1 and S2). The slippery sequence is represented in a box. (C) (SEQ ID NO: 29 and SEQ ID NO: 30) An alternative model taking into account the sequence of nucleotide 2489 to 2493 in the folding of the pseudoknot. This structure contains an additional complementarity sequence (stem) section. (D) Schematic representation of the pseudoknot, in which the three stems are marked: S1, S2 and S3.

Please delete the paragraph on page 6, lines 6-18, and replace it with the following paragraph:

Figure 17 shows an outline of the method for the obtainment of vaccinal viruses by transfection of infected cells with RNA DI-C. A prototype outline is illustrated with the construction that enabled the production of DI-C RNA by *in vitro* transcription, maintaining the 5' and 3' ends present in the original defective particle. The sequence of the T7 promoter [PrT7] (SEQ ID NO: 31) and the sequence of the autocatalytic ribozyme of the hepatitis delta virus (HDV) [Rz HDV] (SEQ ID NO: 32) were cloned

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flanking the DI-C RNA sequence. The position of the autocatalytic cleavage introduced by the ribozyme is marked above the sequence. The arrows indicate the positions of the internal transcription promoter sequences maintained in a natural form in the RNA DI-C. L[[,]]: leader. T7ø [[,]]: T7 bacteriophage transcription termination signals. Virions encapsidating both the helper virus as well as the defective genomes in which the heterologous genes had been cloned were recovered, when the *in vitro* transcribed RNAs were transfected into ST cells infected with the corresponding helper virus.

Please associate the Replacement Sequence Listing, filed concurrently, at the end of the specification.

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